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Conference Abstract

What can be Concluded from COI Gene Data in Limited History Specimen: A sample analysis of a forest pest, *Lymantria dispar*

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Abstract

Nowadays, more and more biodiversity and biogeography studies are conducted with the help of gene sequences. Fresh samples obtained using consistent collection methods can provide DNA for analysis and yield the current status of target species. As there are often no historical samples providing a timescale, it is often difficult to draw conclusions and to provide an evolutionary explanation of the observed biogeographical patterns because of a lack of evidence. The huge natural history specimen collections in museums could possibly provide this information.

The gypsy moth, *Lymantria dispar* (Linnaeus) is a worldwide forest pest species. Our analyses of mitochondrial COI gene sequencing data in specimens from disparate locations revealed previously unknown genetic relationships in gypsy moth populations across space (in and around China) and time (1955–2012). We recovered 103 full-length COI gene sequences from eight fresh samples and from 95 *Lymantria dispar* collection specimens that had been captured between 1955 and 1996. Combining 103 full-length COI gene sequences with 146 COI gene sequences from Genbank (https://www.ncbi.nlm.nih.gov) or DNA barcode libraries, we analyzed the genetic differentiation,

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gene flow and haplotypes (special sequences from individuals) within the gypsy moth populations in order to reflect the genetic structure and population dynamics of this pest.

Twenty-five previously unknown haplotypes were discovered. Regional populations from the same location, but collected at different times, showed high genetic diversity. In some geographical populations (Heilongjiang, Liaoning and Beijing populations), the genetic differentiation was greatest in 1979, but much lower in 1992 and 2012.

This study is an example that shows how specimen collections can be useful to complete gaps in biodiversity studies carried out through genetic sequencing.

Keywords

Lymantria dispar specimens, COI gene, biogeopraphy

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